

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 23, 2005, 23:05:16 ; Search time 1868 Seconds
(without alignments)
427.917 Million cell updates/sec

Title: US-10-646-436-10

Perfect score: 21

Sequence: 1 gcagcagagucuccauctt 21

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	19.4	92.4	532	9	CE099065 tigr-gss-
C 2	19.4	92.4	573	2	BF921577 MR1-NT017
C 3	19.4	90.5	85	2	AW276802 XP66a01.x
C 4	19.4	90.5	100	2	BF920141 MR1-NT017
C 5	19.4	90.5	102	4	BF958934 PM1-NN120
C 6	19.4	90.5	119	2	AW901233 CM4-NN101
C 7	19.4	90.5	124	4	BM821731 K-EST0090
C 8	19.4	90.5	136	6	CD612966 56043322J
C 9	19.4	90.5	137	6	CD612965 56043322H
C 10	19.4	90.5	138	5	BQ339862 PM1-NN120
C 11	19.4	90.5	142	7	D45267 HUMHG1194 H
C 12	19.4	90.5	147	5	BQ339466 PM1-NN120
C 13	19.4	90.5	148	2	BF946357 PM1-EN006
C 14	19.4	90.5	149	7	R47195 CBS-309 Sub
C 15	19.4	90.5	169	2	BE766895 RC2-NT011
C 16	19.4	90.5	177	1	AL048592 DKFp5586H
C 17	19.4	90.5	183	4	BI032792 MR4-NN018
C 18	19.4	90.5	184	4	BF958930 PM1-NN120
C 19	19.4	90.5	185	4	BI036860 MR4-NT014
C 20	19.4	90.5	196	1	AI745406 WC37d01.x
C 21	19.4	90.5	197	4	BI036862 MR4-NT014
C 22	19.4	90.5	201	4	BF957666 PM1-NN120
C 23	19.4	90.5	203	4	BF957653 PM1-NN120
C 24	19.4	90.5	207	4	BF957858 PM1-NN120

25	19	90.5	211	2	BF928116	BF928116 MR4-NT014
C 26	19	90.5	224	2	AW161224	AW161224 au70a10.y
C 27	19	90.5	226	2	BF935119	BF935119 MR4-NT014
C 28	19	90.5	236	4	BF948789	BF948789 MR3-NN021
C 29	19	90.5	238	2	BF923639	BF923639 MR4-NT014
C 30	19	90.5	239	4	EG898974	EG898974 HOA21-1-C
C 31	19	90.5	241	7	CR767137	CR767137 DKFp2469B
C 32	19	90.5	243	1	AA336628	AA336628 EST41242
C 33	19	90.5	244	2	BE766870	BE766870 RC2-NT011
C 34	19	90.5	248	2	BF923643	BF923643 MR4-NT014
C 35	19	90.5	249	4	BF945175	BF945175 PM1-NN120
C 36	19	90.5	250	5	BQ345410	BQ345410 MR4-NT014
C 37	19	90.5	252	2	BF923633	BF923633 MR4-NT014
C 38	19	90.5	252	4	BF963107	BF963107 PM1-NN120
C 39	19	90.5	253	2	BF887875	BF887875 QV2-TN017
C 40	19	90.5	253	4	BI041998	BI041998 MR4-NT014
C 41	19	90.5	256	4	BI041248	BI041248 MR4-NT014
C 42	19	90.5	257	6	CD612964	CD612964 56037472J
C 43	19	90.5	258	4	BF961150	BF961150 PM1-NN120
C 44	19	90.5	258	7	CR763018	CR763018 DKFp2469G
C 45	19	90.5	262	4	BF947155	BF947155 MR3-NN021

ALIGNMENTS

CE099065/c 532 bp DNA linear GSS 24-SBP-2003
tigr-gss-dog-17000371093708 Dog Library Canis familiaris genomic,
genomic survey sequence.
CE099065
CE099065.1 GI:35165950
GSS.
Canis familiaris (dog)
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 532)
AUTHORS Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
TITLE The dog genome: survey sequencing and comparative analysis
JOURNAL Science 301 (5641), 1898-1903 (2003)
MEDLINE 22875432
PUBMED 14512627
COMMENT Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirkness@tigr.org
Class: shotgun.
Location/Qualifiers
1. 532
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site 1: BstXI; Libraries were prepared from
peripheral blood"

Query Match 92.4%; Score 19.4; DB 9; Length 532;
Best Local Similarity 76.2%; Pred. No. 2.1e+02;
Matches 16; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
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Db 82 GCAGCAGAGTCTACATCATTT 62

/clone_lib="NN1011"
 /note="Organ: nervous normal; Vector: puc18; Site_1: SmaI;
 Site_2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

ORIGIN

Query Match 90.5%; Score 19; DB 2; Length 119;
 Best Local Similarity 73.7%; Pred. No. 2.5e+02;
 Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GCAGCAGAGUCUUCACAU 19
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 Db 101 GCAGCAGAGTCTTCATCAT 83

RESULT 7

BM821731/c
 LOCUS BM821731 124 bp mRNA linear EST 06-MAR-2002
 DEFINITION K-EST0090952 S20T665307 Homo sapiens cDNA clone S20T665307-15-H01
 5' mRNA sequence.
 ACCESSION BM821731
 VERSION BM821731.1 GI:19178144
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 124)
 Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.

TITLE 21C Frontier Korean EST Project 2001

JOURNAL
COMMENT

Unpublished (2002)
 Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 15 row: H column: 01
 High quality sequence stop: 124.

FEATURES

source

1..124
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="S20T665307-15-H01"
 /sex="M"
 /lab_host="Top10F"
 /clone_lib="S20T665307"

/note="Organ: Stomach; Vector: pCNS; Site_1: EcoRI;
 Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
 bacterial alkaline phosphatase (BAP) and then decapped
 with tobacco acid pyrophosphatase (TAP). The decapped
 intact mRNA was ligated with DNA-RNA linker including EcoR
 I site by treatment of T4 RNA ligase and the first strand
 cDNA was synthesized from oligo dt-selected mRNA by
 priming with dt-tailed vector. The dt-tailed vector was
 adjusted to have about 60nt. The cDNA vector was
 circularized with E. coli DNA ligase after digestion of
 EcoRI which site is also included in vector. An RNA strand
 converted to a DNA strand by Okayama-Berg method. The
 obtained cDNA vectors were used for transposition of
 competent cells E. coli Top10F by electroporation method.
 The cDNA libraries constructed by this method are
 full-length enriched cDNA library."

ORIGIN

Query Match 90.5%; Score 19; DB 4; Length 124;
 Best Local Similarity 73.7%; Pred. No. 2.5e+02;
 Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GCAGCAGAGUCUUCACAU 19
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 Db 100 GCAGCAGAGTCTTCATCAT 82

RESULT 8

CD612966
 LOCUS CD612966 136 bp mRNA linear EST 12-JAN-2004
 DEFINITION S6043322J1 FLP Homo sapiens cDNA, mRNA sequence.
 ACCESSION CD612966
 VERSION CD612966.1 GI:40261230
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 136)
 Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
 Circular rapid amplification of cDNA ends for high-throughput
 extension cloning of partial genes
 Genomics 84 (1), 205-210 (2004)

JOURNAL

COMMENT

Contact: Fu GK
 Incyte Genomics, Inc.
 3160 Porter Dr., Palo Alto, CA 94304, USA
 Tel: 6508454102
 Email: gfu@incyte.com.

FEATURES

source

1..136
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone_lib="FLP"
 /note="Vector: pDrive Cloning Vector"

ORIGIN

Query Match 90.5%; Score 19; DB 6; Length 136;
 Best Local Similarity 73.7%; Pred. No. 2.6e+02;
 Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GCAGCAGAGUCUUCACAU 19
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 Db 71 GCAGCAGAGTCTTCATCAT 89

FEATURES

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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="S20T665307-15-H01"
 /sex="M"
 /lab_host="Top10F"
 /clone_lib="S20T665307"

/note="Organ: Stomach; Vector: pCNS; Site_1: EcoRI;
 Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
 bacterial alkaline phosphatase (BAP) and then decapped
 with tobacco acid pyrophosphatase (TAP). The decapped
 intact mRNA was ligated with DNA-RNA linker including EcoR
 I site by treatment of T4 RNA ligase and the first strand
 cDNA was synthesized from oligo dt-selected mRNA by
 priming with dt-tailed vector. The dt-tailed vector was
 adjusted to have about 60nt. The cDNA vector was
 circularized with E. coli DNA ligase after digestion of
 EcoRI which site is also included in vector. An RNA strand
 converted to a DNA strand by Okayama-Berg method. The
 obtained cDNA vectors were used for transposition of
 competent cells E. coli Top10F by electroporation method.
 The cDNA libraries constructed by this method are
 full-length enriched cDNA library."

ORIGIN

CD612965/c
 LOCUS CD612965 137 bp mRNA linear EST 12-JAN-2004
 DEFINITION S6043322H1 FLP Homo sapiens cDNA, mRNA sequence.
 ACCESSION CD612965
 VERSION CD612965.1 GI:40261229
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 137)
 Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
 Circular rapid amplification of cDNA ends for high-throughput
 extension cloning of partial genes
 Genomics 84 (1), 205-210 (2004)

JOURNAL

COMMENT

Contact: Fu GK
 Incyte Genomics, Inc.
 3160 Porter Dr., Palo Alto, CA 94304, USA
 Tel: 6508454102
 Email: gfu@incyte.com.

FEATURES

source

1..137
 /organism="Homo sapiens"
 /mol_type="mRNA"

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/db_xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"

ORIGIN
Query Match          90.5%; Score 19; DB 6; Length 137;
Best Local Similarity 73.7%; Pred. No. 2.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY   1 GCAGCAGAGUCUUAUCAU 19
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Db    66 GCAGCAGAGTCTTCATCAT 48

RESULT 10
LOCUS       BQ339862                138 bp     mRNA         linear        EST 20-MAY-2002
DEFINITION PM1-NN1200-011200-010-f07 NN1200 Homo sapiens cDNA, mRNA sequence.
ACCESSION  BQ339862
VERSION    BQ339862.1 GI:20999978
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 138)
AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.P., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
JOURNAL    Proc.Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE    20202663
PUBMED     10737800
COMMENT    Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?ti=PM1&t2=PM1-NN1200-011200-010-f07&t3=2000-12-01&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 17
            High quality sequence stop: 35.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="NN1200"
                     /note="Organ: nervous normal; Vector: puc18; Site 1: SmaI; Site 2: SnaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN
Query Match          90.5%; Score 19; DB 5; Length 138;
Best Local Similarity 73.7%; Pred. No. 2.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY   1 GCAGCAGAGUCUUAUCAU 19
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Db    66 GCAGCAGAGTCTTCATCAT 48

RESULT 11
LOCUS       D45267/c              142 bp     mRNA         linear        EST 30-DEC-1995
DEFINITION HUMHG1194 Human cerebral cortex Homo sapiens cDNA, mRNA sequence.
ACCESSION  D45267
VERSION    D45267.1 GI:1136645
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 142)
AUTHORS   Takahashi,N., Hashida,H., Zhao,N., Mizumi,Y. and Sakaki,Y.
TITLE     High-density cDNA filter analysis of the expression profiles of the genes preferentially expressed in human brain
JOURNAL    Gene 164, 219-227 (1995)
MEDLINE    96069586
PUBMED     7590334
COMMENT    Contact: Nobuaki Takahashi
            Institute of Medical Science
            University of Tokyo
            Shirokanedai 4-6-1, Minato-ku, Tokyo, Japan 108
            Tel: 03-5449-5625
            Fax: 03-5449-5445
FEATURES             Location/Qualifiers
     source           1..142
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="Human cerebral cortex"
                     /note="Adult male cerebral cortex tissue."

ORIGIN
Query Match          90.5%; Score 19; DB 7; Length 142;
Best Local Similarity 73.7%; Pred. No. 2.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY   1 GCAGCAGAGUCUUAUCAU 19
      |||||:::||:|:~
Db    77 GCAGCAGAGTCTTCATCAT 59

RESULT 12
LOCUS       BQ339466                147 bp     mRNA         linear        EST 20-MAY-2002
DEFINITION PM1-NN1200-051100-004-h12 NN1200 Homo sapiens cDNA, mRNA sequence.
ACCESSION  BQ339466
VERSION    BQ339466.1 GI:20999152
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 147)
AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
JOURNAL    Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE    20202663
PUBMED     10737800
COMMENT    Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

```

Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?cl=PM1&t2=PM1-NN1200-051100-004-h12&t3=2000-11-05&t4=1>)
Seq primer: puc 18 forward
High quality sequence start: 14
High quality sequence stop: 34.

FEATURES

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Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mrna"
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/dev_stage="Adult"
/clone_lib="NN1200"
/note="Organ: nervous normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 90.5%; Score 19; DB 5; Length 147;
Best Local Similarity 73.7%; Pred. No. 2.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGCAGAGUCUUCAUCAU 19
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Db 124 GCAGCAGAGTCTTCATCAT 142

RESULT 13
BF846357
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?cl=PM1&t2=PM1-EN0065-231000-002-b01&t3=2000-10-23&t4=1>)
Seq primer: puc 18 forward
High quality sequence stop: 110.

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?cl=PM1&t2=PM1-EN0065-231000-002-b01&t3=2000-10-23&t4=1>)
Seq primer: puc 18 forward
High quality sequence stop: 110.

FEATURES

source
1..148
Location/Qualifiers
1..148
/organism="Homo sapiens"
/mol_type="mrna"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="EN0065"
/note="Organ: lung_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 90.5%; Score 19; DB 2; Length 148;
Best Local Similarity 73.7%; Pred. No. 2.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGCAGAGUCUUCAUCAU 19
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Db 36 GCAGCAGAGTCTTCATCAT 54

RESULT 14

R47195/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Coca-Prados, M.
Department of Ophthalmology and Visual Science
Yale University Medical School
330 Cedar Street, New Haven, CT 06520-8061
Tel: 2037852742
Fax: 2037856123
Email: miguel.coca-prados@quickmail.yale.edu
Seq primer: T3.

FEATURES

source
1..149
Location/Qualifiers
1..149
/organism="Homo sapiens"
/mol_type="mrna"
/db_xref="taxon:9606"
/clone_lib="CBS-389"
/note="Vector: pBlueScript II SK; Site 1: EcoRI; Site 2: XhoI; A subtractive cDNA library was developed by hybridizing antisense, single-stranded phagemid DNA (ssDNA) (as pBlueScript SK-) from the ocular ciliary body cDNA library (target) of a 34-year-old female donor in lambda-Uni-ZAP XR with biotinylated sense RNA of an ocular cell line cDNA library (driver) in the same vector."

ORIGIN

Query Match 90.5%; Score 19; DB 7; Length 149;
Best Local Similarity 73.7%; Pred. No. 2.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGCAGAGUCUUCAU 19
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 Db 69 GCAGCAGAGTCTTCATCAT 51

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 LOCUS RC2-NT0110-050600-013-f03 NT0110 Homo sapiens cDNA, mRNA sequence.
 DEFINITION BE766895
 ACCESSION BE766895
 VERSION BE766895.1 GI:10196819
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 169)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
 Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
 O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 PUBMED 10737800
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC2-NT0110-050
 600-013-f03&t3=2000-06-05&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 18
 High quality sequence stop: 169.

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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="NT0110"
 /note="Organ: nervous tumor; Vector: puc18; Site_1: SmaI;
 Site_2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

ORIGIN
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 Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGCAGAGUCUUCAU 19
 |||||:|:|:|:
 Db 57 GCAGCAGAGTCTTCATCAT 39

Search completed: May 24, 2005, 00:21:54
 Job time : 1874 secs

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C 3	19	90.5	181	5	PT-0895-02303-18	Sequence 18, Appl
C 4	19	90.5	195	2	US-08-485-657A-14	Sequence 14, Appl
C 5	19	90.5	195	4	US-09-366-380A-14	Sequence 14, Appl
C 6	19	90.5	195	5	PT-0895-02303-14	Sequence 14, Appl
C 7	19	90.5	275	4	US-09-513-999C-11015	Sequence 1015, A
C 8	19	90.5	396	4	US-09-640-173-15	Sequence 15, Appl
C 9	19	90.5	396	4	US-09-713-550-15	Sequence 15, Appl
C 10	19	90.5	396	4	US-09-825-294-15	Sequence 15, Appl
C 11	19	90.5	396	4	US-09-970-966-15	Sequence 15, Appl
C 12	19	90.5	482	4	US-09-621-976-13267	Sequence 13267, A
C 13	19	90.5	491	4	US-09-513-999C-3749	Sequence 3749, Ap
C 14	19	90.5	601	4	US-09-949-016-201815	Sequence 201815,
C 15	19	90.5	1648	3	US-09-659-791A-3	Sequence 3, Appli
C 16	19	90.5	1625	3	US-09-659-791A-13	Sequence 13, Appl
C 17	19	90.5	1825	4	US-09-949-016-5661	Sequence 5661, Ap
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C 19	19	90.5	17348	4	US-09-949-016-17403	Sequence 17403, A
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C 21	16.8	80.0	334	3	US-09-227-357-90	Sequence 90, Appl
C 22	16.8	80.0	462	4	US-09-328-352-1618	Sequence 1618, Ap
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C 24	16.8	80.0	75378	4	US-09-949-016-17140	Sequence 17140, A
C 25	16.8	80.0	117001	4	US-09-949-016-15684	Sequence 15684, A
C 26	16.4	78.1	183112	4	US-09-949-016-14184	Sequence 14184, A
C 27	16.2	77.1	332	4	US-09-410-935B-6	Sequence 6, Appli

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Db          71 GCAGCAGAGTCTTCATCAT 53

RESULT 2
US-09-366-380-19/c
; Sequence 19, Application US/09366380
; Patent No. 6541603
; GENERAL INFORMATION:
; APPLICANT: Kirschling, Deborah J
; APPLICANT: Gudkov, Andrei
; APPLICANT: Roninson, Igor B
; TITLE OF INVENTION: Genes and Genetic Elements Associated
; TITLE OF INVENTION: with Sensitivity to Cisplatin
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive, 32nd Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/366,380
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/199,900
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6541603nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 93,354-N
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 181 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-366-380-19

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Best Local Similarity 73.7%; Pred. No. 21;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy          1 GCAGCAGAGUCUUCAUCAU 19
Db          71 GCAGCAGAGTCTTCATCAT 53

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; Sequence 18, Application PC/TUS9502303
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Genes and Genetic Elements Associated
; TITLE OF INVENTION: with Sensitivity to Cisplatin
; NUMBER OF SEQUENCES: 25
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/02303
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 181 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
PCT-US95-02303-18

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Best Local Similarity 73.7%; Pred. No. 21;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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Db          85 GCAGCAGAGTCTTCATCAT 67

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; Sequence 14, Application US/08485657A
; Patent No. 5942389
; GENERAL INFORMATION:
; APPLICANT: Kirschling, Deborah J
; APPLICANT: Gudkov, Andrei
; APPLICANT: Roninson, Igor B
; TITLE OF INVENTION: Genes and Genetic Elements Associated
; TITLE OF INVENTION: with Sensitivity to Cisplatin
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive, 32nd Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,657A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5942389nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 93,354-N
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 195 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-485-657A-14

Query Match          90.5%; Score 19; DB 2; Length 195;
Best Local Similarity 73.7%; Pred. No. 21;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy          1 GCAGCAGAGUCUUCAUCAU 19
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RESULT 5
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US-09-366-380-14/c
; Sequence 14, Application US/09366380
; Patent No. 6541603
; GENERAL INFORMATION:
; APPLICANT: Kirschling, Deborah J
; APPLICANT: Gudkov, Andrei
; APPLICANT: Roninson, Igor B
; TITLE OF INVENTION: Genes and Genetic Elements Associated
; TITLE OF INVENTION: with Sensitivity to Cisplatin
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive, 32nd Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/366,380
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/199,900
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6541603nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 93,354-N
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 195 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-366-380-14
Query Match 90.5%; Score 19; DB 4; Length 195;
Best Local Similarity 73.7%; Pred. No. 21;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
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Db 85 GCAGCAGAGTCTTCATCAT 67
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; Sequence 14, Application PC/TUS9502303
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Genes and Genetic Elements Associated
; TITLE OF INVENTION: with Sensitivity to Cisplatin
; NUMBER OF SEQUENCES: 25
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02303
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 195 base pairs

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
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Best Local Similarity 73.7%; Pred. No. 21;
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US-09-513-999C-11015/c
; Sequence 11015, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A. Y.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 11015
; LENGTH: 275
; TYPE: DNA
; ORGANISM: Homo sapiens
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Db 126 GCAGCAGAGTCTTCATCAT 108
RESULT 8
US-09-640-173-15/c
; Sequence 15, Application US/09640173
; Patent No. 6613515
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: OVARIAN TUMOR SEQUENCES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 210121.484C2
; CURRENT APPLICATION NUMBER: US/09/640,173
; CURRENT FILING DATE: 2000-08-15
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(396)
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; Patent No. 6617109
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C4
; CURRENT APPLICATION NUMBER: US/09/713,550
; CURRENT FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapien
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; NAME/KEY: misc_feature
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; OTHER INFORMATION: n = A,T,C or G
US-09-713-550-15

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Best Local Similarity 73.7%; Pred. No. 24;
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Db 77 GCAGCAGAGTCTTCATCAT 59

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US-09-825-294-15/c
; Sequence 15, Application US/09825294
; Patent No. 6710170
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825,294
; CURRENT FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(396)
; OTHER INFORMATION: n = A,T,C or G
US-09-825-294-15

Query Match 90.5%; Score 19; DB 4; Length 396;
Best Local Similarity 73.7%; Pred. No. 24;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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Db 77 GCAGCAGAGTCTTCATCAT 59

Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

RESULT 11
US-09-970-966-15/c
; Sequence 15, Application US/09970966
; Patent No. 6720146
; GENERAL INFORMATION:
; APPLICANT: Stolk, John A.
; APPLICANT: Molesh, David Alan
; APPLICANT: Fling, Steven P.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C6
; CURRENT APPLICATION NUMBER: US/09/970,966
; CURRENT FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 333_
; OTHER INFORMATION: n = A,T,C or G
US-09-970-966-15

Query Match 90.5%; Score 19; DB 4; Length 396;
Best Local Similarity 73.7%; Pred. No. 24;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGCAGAGUCUUCACAU 19
|||||||:|:~|:|:~|:
Db 77 GCAGCAGAGTCTTCATCAT 59

RESULT 12

US-09-621-976-13267/c
; Sequence 13267, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 13267
; LENGTH: 482
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-13267

Query Match 90.5%; Score 19; DB 4; Length 482;
Best Local Similarity 73.7%; Pred. No. 24;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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Db 94 GCAGCAGAGTCTTCATCAT 76

RESULT 13

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; Sequence 3749, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.

RESULT 15
US-09-659-791A-3/C

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 23, 2005, 21:40:56 ; Search time 255 Seconds
(without alignments)
487.508 Million cell updates/sec

Title: US-10-646-436-10

Perfect score: 21

Sequence: 1 gcagcagacuccaucautt 21

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Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: Geneseqn1990s:*
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4: Geneseqn2001as:*
5: Geneseqn2001bs:*
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7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	19	90.5	19	12 ADL70523	Adl70523 RNAi for
C 5	19	90.5	19	12 ADL70444	Adl70444 RNAi for
6	19	90.5	19	12 ADL70445	Adl70445 RNAi for
7	19	90.5	21	3 AAA94226	Aaa94226 Human tes
8	19	90.5	21	10 ACF36398	Acf36398 TRPM-2 an
9	19	90.5	21	11 ADM83069	Adm83069 Human TRP
C 10	19	90.5	21	12 ADL70464	Adl70464 RNAi for
C 11	19	90.5	21	12 ADL70430	Adl70430 RNAi for
12	19	90.5	21	12 ADL70406	Adl70406 Antisense
C 13	19	90.5	23	12 ADL70521	Adl70521 Human clu
C 14	19	90.5	195	2 AAT00416	Aat00416 Genetic s
C 15	19	90.5	275	3 AAC06940	Aac06940 Human sec
C 16	19	90.5	396	4 AAF94824	Aaf94824 Human ova
C 17	19	90.5	396	6 ABL48774	AbL48774 Ovarian c
C 18	19	90.5	396	6 ABT03091	Abt03091 Human ova
C 19	19	90.5	396	11 ADM10684	Adm10684 Human ova
C 20	19	90.5	396	12 ADJ11014	Adj11014 Represent

ALIGNMENTS

RESULT 1

ADL70465

ID ADL70465 standard; RNA; 21 BP.

XX AC ADL70465;

XX DT 20-MAY-2004 (first entry)

XX DE RNAi for human clusterin.

XX RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin;

KW cytotostatic; neuroprotective; nontropic; gene silencing; DNA-RNA hybrid;

XX SS.

XX OS Homo sapiens.

XX OS Synthetic.

XX FH Key Location/Qualifiers

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FT /*tag= a

FT /mod_base= OTHER

FT /note= "OTHER= dTdT"

XX WO2004018676-A2.

XX 04-MAR-2004.

XX 21-AUG-2003; 2003WO-CA001277.

XX 21-AUG-2002; 2002US-0405193P.

XX 03-SEP-2002; 2002US-0408152P.

XX 20-MAY-2003; 2003US-0472387P.

XX (UYBR-) UNIV BRITISH COLUMBIA.

XX Jansen B, Gleave ME, Signaevsky M, Beraldi E, Trougakos IP;

XX Gonos ES;

XX WPI; 2004-226852/21.

XX New RNA molecule less than 49 bases and having a sequence effective to

XX mediate degradation or block translation of mRNA that is the

XX transcriptional product of a target gene, useful for treating Alzheimer's

XX PT

XX PT

```
PT disease or cancer.
XX
PS Claim 4; SEQ ID NO 10; 63pp; English.
XX
CC The present sequence is the antisense strand of a short interfering RNA
CC (siRNA) targeted to human clusterin. The sense strand is also provided
CC ADL70464. The siRNA can be used to interfere with the expression of
CC clusterin. Clusterin, also known as testosterone-repressed prostate
CC message-2 (TRPM-2) or sulfated glycoprotein-2 (SGP-2), is expressed in
CC increased amounts by prostate tumour cells following androgen withdrawal,
CC and has also been shown to be critical for neuritic toxicity in mouse
CC models of Alzheimer's disease. siRNAs of the invention can be used alone
CC or in combination with other chemotherapy or apoptosis inducing
CC treatments for the treatment of prostate cancer, sarcomas such as
CC osteosarcoma, renal cell carcinoma, breast cancer, bladder cancer, lung
CC cancer, colon cancer, ovarian cancer, anaplastic large cell lymphoma and
CC melanoma, and also for the treatment of Alzheimer's disease.
XX
SQ Sequence 21 BP; 5 A; 5 C; 4 G; 2 T; 5 U; 0 Other;

Query Match      100.0%; Score 21; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGCAGAGUCUUCAUCAUTT 21
   |||||
DB 1 GCAGCAGAGUCUUCAUCAUTT 21

RESULT 2
ADL70431
ID ADL70431 standard; RNA; 21 BP.
XX
AC ADL70431;
XX
DT 20-MAY-2004 (first entry)
XX
DE RNAi for human clusterin.
XX
KW Human; clusterin; RNAi; melanoma; cytostatic; gene silencing;
KW short interfering RNA; siRNA; DNA-RNA hybrid; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 20..21
FT FT /*tag= a
FT FT /mod_base= OTHER
FT FT /note= "Tt"
XX
PN WO2004018675-A1.
XX
PD 04-MAR-2004.
XX
PF 21-AUG-2003; 2003WO-CA001276.
XX
PR 21-AUG-2002; 2002US-0405193P.
XX
PR 03-SEP-2002; 2002US-0408152P.
XX
PR 02-DEC-2002; 2002US-0319748P.
XX
PR 20-MAY-2003; 2003US-0472387P.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
PA (GLEA/) GLEAVE M E.
XX
PI Jansen B;
XX
DR WPI; 2004-226851/21.
XX
PT Treating melanoma in a mammalian subject comprises administering to the
PT subject a therapeutic agent effective to reduce the effective amount of
PT clusterin in the melanoma cells.
XX
```

```
PS Claim 20; SEQ ID NO 29; 32pp; English.
XX
CC The present sequence is that of a short interfering RNA (siRNA) molecule
CC targeted to human clusterin ADL70403. The invention relates to the
CC treatment of melanoma through reduction in the effective amount of
CC clusterin. The therapeutic agent may be an antisense oligonucleotide
CC ADL70404-ADL70421 or short interfering RNA (siRNA) ADL70422-ADL70445
CC targeted to clusterin. The siRNAs molecules direct cleavage of clusterin
CC mRNA. A method for regulating expression of bcl-xL in a subject or cell
CC line comprises administering an agent effective to modulate the amount of
CC clusterin expression. In clusterin-expressing cells, expression of bcl-xL
CC is down-regulated when the effective amount of clusterin is reduced. Such
CC inhibition is significant because bcl-xL is known to act as an inhibitor
CC of apoptosis.
XX
SQ Sequence 21 BP; 5 A; 5 C; 4 G; 2 T; 5 U; 0 Other;

Query Match      100.0%; Score 21; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGCAGAGUCUUCAUCAUTT 21
   |||||
DB 1 GCAGCAGAGUCUUCAUCAUTT 21

RESULT 3
ADL70522/c
ID ADL70522 standard; RNA; 19 BP.
XX
AC ADL70522;
XX
DT 20-MAY-2004 (first entry)
XX
DE RNAi for human clusterin.
XX
KW RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin;
KW cytostatic; neuroprotective; nontropic; gene silencing; DNA-RNA hybrid;
KW ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 18..19
FT FT /*tag= a
FT FT /mod_base= OTHER
FT FT /note= "OTHER= dtdt"
XX
PN WO2004018676-A2.
XX
PD 04-MAR-2004.
XX
PF 21-AUG-2003; 2003WO-CA001277.
XX
PR 21-AUG-2002; 2002US-0405193P.
XX
PR 03-SEP-2002; 2002US-0408152P.
XX
PR 20-MAY-2003; 2003US-0472387P.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI Jansen B, Gleave ME, Signaevsky M, Beraldi E, Trougakos IP;
PI Gonos ES;
XX
DR WPI; 2004-226852/21.
XX
PT New RNA molecule less than 49 bases and having a sequence effective to
PT mediate degradation or block translation of mRNA that is the
PT transcriptional product of a target gene, useful for treating Alzheimer's
PT disease or cancer.
XX
PS Claim 4; SEQ ID NO 67; 63pp; English.
XX
```


CC The present sequence is the sense strand of a short interfering RNA
CC (siRNA) targeted to a specific portion ADL70521 of human clusterin cDNA.
CC The antisense strand is also provided ADL70523. The siRNA can be used to
CC interfere with the expression of clusterin. Clusterin, also known as
CC testosterone-repressed prostate message-2 (TRPM-2) or sulfated
CC glycoprotein-2 (SGP-2), is expressed in increased amounts by prostate
CC tumour cells following androgen withdrawal, and has also been shown to be
CC critical for neuritic toxicity in mouse models of Alzheimer's disease.
CC siRNAs of the invention can be used alone or in combination with other
CC chemotherapies or apoptosis inducing treatments for the treatment of
CC prostate cancer, sarcomas such as osteosarcoma, renal cell carcinoma,
CC breast cancer, bladder cancer, lung cancer, colon cancer, ovarian cancer,
CC anaplastic large cell lymphoma and melanoma, and also for the treatment
CC of Alzheimer's disease. In an example from the invention, the present
CC siRNA was used to examine the effects of clusterin gene silencing in PC-3
CC prostate cancer cells. A reduction in clusterin transcript was observed.
XX
SQ Sequence 19 BP; 5 A; 4 C; 5 G; 0 T; 5 U; 0 Other;

Query Match 90.5%; Score 19; DB 12; Length 19;
Best Local Similarity 73.7%; Pred. No. 33;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGCAGAGUCUUCAUCAU 19
|||||||:|:|:|:|:
DB 19 GCAGCAGAGTCTTCATCAT 1

RESULT 4
ADL70523
ID ADL70523 standard; RNA; 19 BP.
XX
AC ADL70523;
XX
DT 20-MAY-2004 (first entry)
XX
DE RNAi for human clusterin.
XX
KW RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin;
KW cytostatic; neuroprotective; neutropic; gene silencing; DNA-RNA hybrid;
KW ss.
XX Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 18..19
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= dtT"
XX

WO2004018676-A2.
XX
XX
PD 04-MAR-2004.
XX
XX 21-AUG-2003; 2003WO-CA001277.
XX
PR 21-AUG-2002; 2002US-0405193P.
PR 03-SEP-2002; 2002US-0408152P.
PR 20-MAY-2003; 2003US-0472387P.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
XX
XX Jansen B, Gleave ME, Signaevsky M, Beraldi E, Trougakos IP;
PI Gonos ES;
XX
XX WPI; 2004-226852/21.
XX

XX New RNA molecule less than 49 bases and having a sequence effective to
PT mediate degradation or block translation of mRNA that is the
PT transcriptional product of a target gene, useful for treating Alzheimer's
PT disease or cancer.
XX

PS Claim 4; SEQ ID NO 68; 63pp; English.
XX
CC The present sequence is the antisense strand of a short interfering RNA
CC (siRNA) targeted to a specific portion ADL70521 of human clusterin cDNA.
CC The sense strand is also provided ADL70522. The siRNA can be used to
CC interfere with the expression of clusterin. Clusterin, also known as
CC testosterone-repressed prostate message-2 (TRPM-2) or sulfated
CC glycoprotein-2 (SGP-2), is expressed in increased amounts by prostate
CC tumour cells following androgen withdrawal, and has also been shown to be
CC critical for neuritic toxicity in mouse models of Alzheimer's disease.
CC siRNAs of the invention can be used alone or in combination with other
CC chemotherapies or apoptosis inducing treatments for the treatment of
CC prostate cancer, sarcomas such as osteosarcoma, renal cell carcinoma,
CC breast cancer, bladder cancer, lung cancer, colon cancer, ovarian cancer,
CC anaplastic large cell lymphoma and melanoma, and also for the treatment
CC of Alzheimer's disease. In an example from the invention, the present
CC siRNA was used to examine the effects of clusterin gene silencing in PC-3
CC prostate cancer cells. A reduction in clusterin transcript was observed.
XX
SQ Sequence 19 BP; 5 A; 5 C; 4 G; 0 T; 5 U; 0 Other;

Query Match 90.5%; Score 19; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGCAGAGUCUUCAUCAU 19
|||||||:|:|:|:|:
DB 1 GCAGCAGAGUCUUCAUCAU 19

RESULT 5
ADL70444/C
ID ADL70444 standard; RNA; 19 BP.
XX
AC ADL70444;
XX
DT 20-MAY-2004 (first entry)
XX
DE RNAi for human clusterin.
XX
KW Human; clusterin; RNAi; melanoma; cytostatic; gene silencing;
KW short interfering RNA; siRNA; DNA-RNA hybrid; ss.
XX Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 18..19
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= TT"
XX

WO2004018675-A1.
XX
XX
PD 04-MAR-2004.
XX
XX 21-AUG-2003; 2003WO-CA001276.
XX
PR 21-AUG-2002; 2002US-0405193P.
PR 03-SEP-2002; 2002US-0408152P.
PR 02-DEC-2002; 2002US-0319748P.
PR 20-MAY-2003; 2003US-0472387P.
XX
XX (UYBR-) UNIV BRITISH COLUMBIA.
PA (GLEA/) GLEAVE M E.
XX
XX Jansen B;
XX

XX WPI; 2004-226851/21.
XX
XX Treating melanoma in a mammalian subject comprises administering to the
PT subject a therapeutic agent effective to reduce the effective amount of
PT clusterin in the melanoma cells.
XX

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XX PS Claim 20; SEQ ID NO 42; 32pp; English.
XX CC The present sequence is that of a short interfering RNA (siRNA) molecule
XX CC targeted to human clusterin ADL70403. The invention relates to the
XX CC treatment of melanoma through reduction in the effective amount of
XX CC clusterin. The therapeutic agent may be an antisense oligonucleotide
XX CC ADL70404-ADL70421 or short interfering RNA (siRNA) ADL70422-ADL70445
XX CC targeted to clusterin. The siRNAs molecules direct cleavage of clusterin
XX CC mRNA. A method for regulating expression of bcl-xL in a subject or cell
XX CC line comprises administering an agent effective to modulate the amount of
XX CC clusterin expression. In clusterin-expressing cells, expression of bcl-xL
XX CC is down-regulated when the effective amount of clusterin is reduced. Such
XX CC inhibition is significant because bcl-xL is known to act as an inhibitor
XX CC of apoptosis.
XX SQ Sequence 19 BP; 5 A; 4 C; 5 G; 0 T; 5 U; 0 Other;
      Query Match      90.5%; Score 19; DB 12; Length 19;
      Best Local Similarity 73.7%; Pred. No. 33;
      Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGCAGAGUCUUCUCAU 19
Db 19 GCAGCAGAGTCTTCATCAT 1

RESULT 6
ID ADL70445 standard; RNA; 19 BP.
XX AC ADL70445;
XX DT 20-MAY-2004 (first entry)
XX DE RNAi for human clusterin.
XX KW Human; clusterin; RNAi; melanoma; cytostatic; gene silencing;
XX KW short interfering RNA; siRNA; DNA-RNA hybrid; ss.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT modified_base 18..19 /*tag= a
XX -FT /mod_base= OTHER
XX FT /note= "OTHER= TT"
XX PN WO2004018675-A1.
XX PD 04-MAR-2004.
XX PF 21-AUG-2003; 2003WO-CA001276.
XX PR 21-AUG-2002; 2002US-0405193P.
XX PR 03-SEP-2002; 2002US-0408152P.
XX PR 02-DEC-2002; 2002US-0319748P.
XX PR 20-MAY-2003; 2003US-0472387P.
XX PA (UYBR-) UNIV BRITISH COLUMBIA.
XX PA (GLEA/) GLEAVE M E.
XX PI Jansen B;
XX WPI; 2004-226851/21.
XX DR Treating melanoma in a mammalian subject comprises administering to the
XX PT subject a therapeutic agent effective to reduce the effective amount of
XX PT clusterin in the melanoma cells.
XX PS Claim 20; SEQ ID NO 43; 32pp; English.
XX
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```
CC The present sequence is that of a short interfering RNA (siRNA) molecule
CC targeted to human clusterin ADL70403. The invention relates to the
CC treatment of melanoma through reduction in the effective amount of
CC clusterin. The therapeutic agent may be an antisense oligonucleotide
CC ADL70404-ADL70421 or short interfering RNA (siRNA) ADL70422-ADL70445
CC targeted to clusterin. The siRNAs molecules direct cleavage of clusterin
CC mRNA. A method for regulating expression of bcl-xL in a subject or cell
CC line comprises administering an agent effective to modulate the amount of
CC clusterin expression. In clusterin-expressing cells, expression of bcl-xL
CC is down-regulated when the effective amount of clusterin is reduced. Such
CC inhibition is significant because bcl-xL is known to act as an inhibitor
CC of apoptosis.
XX SQ Sequence 19 BP; 5 A; 5 C; 4 G; 0 T; 5 U; 0 Other;
      Query Match      90.5%; Score 19; DB 12; Length 19;
      Best Local Similarity 100.0%; Pred. No. 33;
      Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGCAGAGUCUUCUCAU 19
Db 1 GCAGCAGAGUCUUCUCAU 19

RESULT 7
ID AAA94226 standard; DNA; 21 BP.
XX AC AAA94226;
XX DT 12-JAN-2001 (first entry)
XX DE Human testosterone-repressed prostate message-2 antisense oligo #2.
XX KW Human; testosterone-repressed prostate message-2; TRPM-2; clusterin;
XX KW sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss.
XX OS Homo sapiens.
XX PN WO200049937-A2.
XX PD 31-AUG-2000.
XX PF 25-FEB-2000; 2000WO-US004875.
XX PR 26-FEB-1999; 99US-0121726P.
XX PA (UYBR-) UNIV BRITISH COLUMBIA.
XX PI Gleave M, Rennie PS, Miyake H, Nelson C;
XX WPI; 2000-533132/48.
XX PT Treating prostatic tumors and renal cancers by antisense inhibition of
XX PT the testosterone-repressed prostate messenger-2 gene.
XX PS Claim 3; Page 36; 38pp; English.
XX CC The present sequence is an antisense oligonucleotide directed at the
XX CC human testosterone-repressed prostate message-2 (TRPM-2, also known as
XX CC clusterin, sulfated glycoprotein-2 or SGP-2). The sequence was shown to
XX CC promote the regression of tumours, and oligonucleotides directed at human
XX CC TRPM-2 can be used in the treatment of tumour cells expressing the TRPM-2
XX CC gene. These include prostate cancer, renal cell cancer and some breast
XX CC cancer cells. In addition to this, they also increase the
XX CC chemosensitivity of the cells, meaning that conventional chemotherapy is
XX CC more effective
XX SQ Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 U; 0 Other;
      Query Match      90.5%; Score 19; DB 3; Length 21;
      Best Local Similarity 73.7%; Pred. No. 34;
      Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
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.

```
XX 20-MAY-2004 (first entry)
XX RNAi for human clusterin.
XX
XX RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin;
KW cytosstatic; neuroprotective; nontropic; gene silencing; DNA-RNA hybrid;
KW ss.
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 20..21
XX /*tag= a
XX /mod_base= OTHER
XX /note= "OTHER= dtdt"
XX
XX WO2004018676-A2.
XX
XX 04-MAR-2004.
XX
XX 21-AUG-2003; 2003WO-CA001277.
XX
XX 21-AUG-2002; 2002US-0405193P.
PR 03-SEP-2002; 2002US-0408152P.
PR 20-MAY-2003; 2003US-0472387P.
XX
XX (UYBR-) UNIV BRITISH COLUMBIA.
XX
XX Jansen B, Gleave ME, Signaevsky M, Beraldi E, Trougakos IP;
PI Gonos ES;
XX
XX WPI; 2004-226852/21.
XX
XX New RNA molecule less than 49 bases and having a sequence effective to
XX mediate degradation or block translation of mRNA that is the
XX transcriptional product of a target gene, useful for treating Alzheimer's
XX disease or cancer.
XX
XX Claim 4; SEQ ID NO 9; 63pp; English.
XX
XX The present sequence is the sense strand of a short interfering RNA
XX (siRNA) targeted to human clusterin. The antisense strand is also
XX provided ADL70465. The siRNA can be used to interfere with the expression
XX of clusterin. Clusterin, also known as testosterone-repressed prostate
XX message-2 (TRPM-2) or sulfated glycoprotein-2 (SGP-2), is expressed in
XX increased amounts by prostate tumour cells following androgen withdrawal,
XX and has also been shown to be critical for neuritic toxicity in mouse
XX models of Alzheimer's disease. siRNAs of the invention can be used alone
XX or in combination with other chemotherapy or apoptosis inducing
XX treatments for the treatment of prostate cancer, sarcomas such as
XX osteosarcoma, renal cell carcinoma, breast cancer, bladder cancer, lung
XX cancer, colon cancer, ovarian cancer, anaplastic large cell lymphoma and
XX melanoma, and also for the treatment of Alzheimer's disease.
XX
XX Sequence 21 BP; 5 A; 4 C; 5 G; 2 T; 5 U; 0 Other;
SQ
Query Match 90.5%; Score 19; DB 12; Length 21;
Best Local Similarity 73.7%; Pred. No. 34;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCACGAGAGUCUUCAUCAU 19
DB 19 GCACGAGAGTCTTCATCAT 1
RESULT 11
ADL70430/c
ID ADL70430 standard; RNA; 21 BP.
XX
XX ADL70430;
XX
```

```
DT 20-MAY-2004 (first entry)
XX RNAi for human clusterin.
DE
XX
XX Human; clusterin; RNAi; melanoma; cytostatic; gene silencing;
KW short interfering RNA; siRNA; DNA-RNA hybrid; ss.
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 20..21
XX /*tag= a
XX /mod_base= OTHER
XX /note= "OTHER= TT"
XX
XX WO2004018675-A1.
XX
XX 04-MAR-2004.
XX
XX 21-AUG-2003; 2003WO-CA001276.
XX
XX 21-AUG-2002; 2002US-0405193P.
PR 03-SEP-2002; 2002US-0408152P.
PR 02-DEC-2002; 2002US-0319748P.
PR 20-MAY-2003; 2003US-0472387P.
XX
XX (UYBR-) UNIV BRITISH COLUMBIA.
XX (GLEA/) GLEAVE M E.
XX
XX Jansen B;
XX
XX WPI; 2004-226851/21.
XX
XX Treating melanoma in a mammalian subject comprises administering to the
XX subject a therapeutic agent effective to reduce the effective amount of
XX clusterin in the melanoma cells.
XX
XX Claim 20; SEQ ID NO 28; 32pp; English.
XX
XX The present sequence is that of a short interfering RNA (siRNA) molecule
XX targeted to human clusterin ADL70403. The invention relates to the
XX treatment of melanoma through reduction in the effective amount of
XX clusterin. The therapeutic agent may be an antisense oligonucleotide
XX ADL70404-ADL70421 or short interfering RNA (siRNA) ADL70422-ADL70445
XX targeted to clusterin. The siRNAs molecules direct cleavage of clusterin
XX mRNA. A method for regulating expression of bcl-xL in a subject or cell
XX line comprises administering an agent effective to modulate the amount of
XX clusterin expression. In clusterin-expressing cells, expression of bcl-xL
XX is down-regulated when the effective amount of clusterin is reduced. Such
XX inhibition is significant because bcl-xL is known to act as an inhibitor
XX of apoptosis.
XX
XX Sequence 21 BP; 5 A; 4 C; 5 G; 2 T; 5 U; 0 Other;
SQ
Query Match 90.5%; Score 19; DB 12; Length 21;
Best Local Similarity 73.7%; Pred. No. 34;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCACGAGAGUCUUCAUCAU 19
DB 19 GCACGAGAGTCTTCATCAT 1
RESULT 12
ADL70406
ID ADL70406 standard; DNA; 21 BP.
XX
XX ADL70406;
XX
XX 20-MAY-2004 (first entry)
XX
XX Antisense oligonucleotide to human clusterin.
DE
```

XX Human; clusterin; antisense; melanoma; cytosstatic; gene silencing; ss.
XX Homo sapiens.
OS Synthetic.
XX Key Location/Qualifiers
FH modified_base 1..21 /*tag= b
FT /mod_base= OTHER
FT /note= "OTHER= phosphorothioate nucleotides"
FT modified_base 1..4 /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= 2'-O-methoxyethyl modifications"
FT modified_base 18..21 /*tag= c
FT /mod_base= OTHER
FT /note= "OTHER= 2'-O-methoxyethyl modifications"
XX WO2004018675-A1.
XX 04-MAR-2004.
XX 21-AUG-2003; 2003WO-CA001276.
XX 21-AUG-2002; 2002US-0405193P.
XX 03-SEP-2002; 2002US-0408152P.
XX 02-DEC-2002; 2002US-0319748P.
XX 20-MAY-2003; 2003US-0472387P.
XX (UYBR-) UNIV BRITISH COLUMBIA.
XX (GLEA/) GLEAVE M E.
XX Jansen B;
XX WPI; 2004-226851/21.
XX Treating melanoma in a mammalian subject comprises administering to the
XX subject a therapeutic agent effective to reduce the effective amount of
XX clusterin in the melanoma cells.
XX Claim 7; SEQ ID NO 4; 32pp; English.
XX The present sequence is that of an antisense oligonucleotide targeted to
XX human clusterin ADL70403. The invention relates to the treatment of
XX melanoma through reduction in the effective amount of clusterin. The
XX therapeutic agent may be an antisense oligonucleotide ADL70404-ADL70421
XX or short interfering RNA (siRNA) ADL70422-ADL70445 targeted to clusterin.
XX The antisense oligonucleotides are complementary to a region of the
XX clusterin mRNA spanning either the translation initiation site or the
XX termination site. They may be modified to increase stability in vivo,
XX e.g. they may be employed as phosphorothioate derivatives and may have 2'
XX -O-(2-methoxyethyl) (MOE) modifications in the 5' and 3' 'wings'. The
XX present antisense oligonucleotide is particularly preferred. It is
XX targeted to the translation initiation codon and next 6 codons of the
XX human clusterin sequence. It has a phosphorothioate backbone throughout
XX and MOE wings, the remaining nucleotides being 2'-deoxynucleotides. In an
XX example from the invention, this antisense oligonucleotide provided a
XX dose-dependent down-regulation of clusterin in human melanoma cells,
XX leading to an increase in apoptotic cell death. In one melanoma cell line
XX (607B) this alone was sufficient to lead to complete cell death. In
XX another melanoma cell line, the surviving cells showed increased
XX sensitivity to subsequent treatment with cisplatin. A claimed method for
XX regulating expression of bcl-xL in a subject or cell line comprises
XX administering an agent effective to modulate the amount of clusterin
XX expression. In clusterin-expressing cells, expression of bcl-xL is down-
XX regulated when the effective amount of clusterin is reduced. Such
XX inhibition is significant because bcl-xL is known to act as an inhibitor
XX of apoptosis.
XX Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 90.5%; Score 19; DB 12; Length 21;
Best Local Similarity 73.7%; Pred. No. 34;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCAGCAGAGUCUUCAU 19
DB 3 GCAGCAGAGTCTTCATCAT 21
|||||:|:|:|:|:
RESULT 13
ADL70521/c
ID ADL70521 standard; cDNA; 23 BP.
XX AC ADL70521;
XX 20-MAY-2004 (first entry)
XX Human clusterin target for RNAi.
XX RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin;
XX cytosstatic; neuroprotective; nontropic; gene silencing; DNA-RNA hybrid;
XX ss.
XX Homo sapiens.
OS Synthetic.
XX WO2004018676-A2.
XX 04-MAR-2004.
XX 21-AUG-2003; 2003WO-CA001277.
XX 21-AUG-2002; 2002US-0405193P.
XX 03-SEP-2002; 2002US-0408152P.
XX 20-MAY-2003; 2003US-0472387P.
XX (UYBR-) UNIV BRITISH COLUMBIA.
XX Jansen B, Gleave ME, Signaevsky M, Beraldi E, Trougakos IP;
XX Gonos ES;
XX WPI; 2004-226852/21.
XX New RNA molecule less than 49 bases and having a sequence effective to
XX mediate degradation or block translation of mRNA that is the
XX transcriptional product of a target gene, useful for treating Alzheimer's
XX disease or cancer.
XX Example 6; SEQ ID NO 66; 63pp; English.
XX The present sequence is a human clusterin cDNA target for a double-
XX stranded short interfering RNA (siRNA) of the invention to demonstrate
XX ADL70523. It was used in an example from the invention to demonstrate
XX clusterin gene silencing in PC-3 prostate cancer cells. Clusterin, also
XX known as testosterone-repressed prostate message-2 (TRPM-2) or sulfated
XX glycoprotein-2 (SGP-2), is expressed in increased amounts by prostate
XX tumour cells following androgen withdrawal, and has also been shown to be
XX critical for neuritic toxicity in mouse models of Alzheimer's disease.
XX siRNAs of the invention can be used alone or in combination with other
XX chemotherapy or apoptosis inducing treatments for the treatment of
XX prostate cancer, sarcomas such as osteosarcoma, renal cell carcinoma,
XX breast cancer, bladder cancer, lung cancer, colon cancer, ovarian cancer,
XX anaplastic large cell lymphoma and melanoma, and also for the treatment
XX of Alzheimer's disease.
XX Sequence 23 BP; 5 A; 5 C; 7 G; 6 T; 0 U; 0 Other;
QY 1 GCAGCAGAGUCUUCAU 19
DB 3 GCAGCAGAGTCTTCATCAT 21
|||||:|:|:|:|:
Query Match 90.5%; Score 19; DB 12; Length 23;
Best Local Similarity 73.7%; Pred. No. 34;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCAGCAGAGUCUUCAU 19
DB 3 GCAGCAGAGTCTTCATCAT 21
|||||:|:~|:|:|:|:

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	Score	Match	†				
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2	21	100.0	21	6	CQ786640	Sequence	CQ786640 Sequence
C 3	19	90.5	19	6	CQ786179	Sequence	CQ786179 Sequence
4	19	90.5	19	6	CQ786180	Sequence	CQ786180 Sequence
C 5	19	90.5	19	6	CQ786653	Sequence	CQ786653 Sequence
6	19	90.5	19	6	CQ786654	Sequence	CQ786654 Sequence
C 7	19	90.5	21	6	CQ786121	Sequence	CQ786121 Sequence
8	19	90.5	21	6	CQ786615	Sequence	CQ786615 Sequence
C 9	19	90.5	21	6	CQ786639	Sequence	CQ786639 Sequence
C 10	19	90.5	23	6	CQ786178	Sequence	CQ786178 Sequence
C 11	19	90.5	181	6	AR302789	Sequence	AR302789 Sequence
C 12	19	90.5	195	6	AR302784	Sequence	AR302784 Sequence
C 13	19	90.5	255	6	CQ693037	Sequence	CQ693037 Sequence
C 14	19	90.5	270	6	CQ688092	Sequence	CQ688092 Sequence
C 15	19	90.5	275	6	AX895152	Sequence	AX895152 Sequence
C 16	19	90.5	275	6	BD030685	Sequence	BD030685 Sequence
C 17	19	90.5	306	6	CQ684015	Sequence	CQ684015 Sequence
C 18	19	90.5	396	6	AR391192	Sequence	AR391192 Sequence
C 19	19	90.5	396	6	AR392897	Sequence	AR392897 Sequence

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RESULT 9

ORIGIN

Search completed: May 23, 2005, 23:50:37
Job time : 1718 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 23, 2005, 23:16:37 ; Search time 341 Seconds
(without alignments)
377.650 Million cell updates/sec

Title: US-10-646-436-10

Perfect score: 21
Sequence: 1 gcagcagagucuccauctt 21

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5695437 seqs, 3066160638 residues

Total number of hits satisfying chosen parameters: 11390874

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	21	100.0	21	17	US-10-646-391A-29
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3	19	90.5	19	17	US-10-646-391A-42
4	19	90.5	19	17	US-10-646-391A-43
5	19	90.5	19	17	US-10-646-436-67
6	19	90.5	19	17	US-10-646-436-68
7	19	90.5	21	9	US-09-944-326-4
8	19	90.5	21	10	US-09-967-726A-4
9	19	90.5	21	16	US-10-080-794-4
10	19	90.5	21	17	US-10-646-391A-4
11	19	90.5	21	17	US-10-646-391A-28

19	90.5	21	17	US-10-646-436-9	Sequence 9, Appli
19	90.5	21	18	US-10-828-394-5	Sequence 5, Appli
19	90.5	21	18	US-10-828-394-5	Sequence 5, Appli
19	90.5	23	17	US-10-646-436-66	Sequence 66, Appli
19	90.5	181	17	US-10-404-579-19	Sequence 19, Appli
19	90.5	195	17	US-10-404-579-14	Sequence 14, Appli
19	90.5	255	17	US-10-242-535A-37963	Sequence 37963, A
19	90.5	255	17	US-10-085-783A-37963	Sequence 37963, A
19	90.5	270	17	US-10-242-535A-33018	Sequence 33018, A
19	90.5	270	17	US-10-085-783A-33018	Sequence 33018, A
19	90.5	306	17	US-10-242-535A-28941	Sequence 28941, A
19	90.5	306	17	US-10-085-783A-28941	Sequence 28941, A
19	90.5	346	19	US-10-696-639-2963	Sequence 2963, Ap
19	90.5	396	9	US-09-825-294-15	Sequence 15, Appl
19	90.5	396	15	US-09-970-966-15	Sequence 15, Appl
19	90.5	396	15	US-10-212-677-15	Sequence 15, Appl
19	90.5	396	17	US-10-361-811-15	Sequence 15, Appl
19	90.5	396	17	US-10-369-186-15	Sequence 15, Appl
19	90.5	461	10	US-09-918-995-32172	Sequence 32172, A
19	90.5	462	10	US-09-918-995-2524	Sequence 2524, A
19	90.5	465	10	US-09-918-995-32177	Sequence 32177, A
19	90.5	490	10	US-09-918-995-12511	Sequence 12511, A
19	90.5	491	10	US-09-918-995-17455	Sequence 17455, A
19	90.5	492	10	US-09-918-995-31156	Sequence 31156, A
19	90.5	704	17	US-10-264-049-1985	Sequence 1985, Ap
19	90.5	1067	19	US-10-491-213-91	Sequence 91, Appl
19	90.5	1117	19	US-10-491-213-93	Sequence 93, Appl
19	90.5	1315	19	US-10-491-213-101	Sequence 101, App
19	90.5	1369	19	US-10-491-213-90	Sequence 90, Appl
19	90.5	1373	19	US-10-491-213-102	Sequence 102, App
19	90.5	1451	16	US-10-133-013-214	Sequence 214, Appl
19	90.5	1568	17	US-10-291-172-29	Sequence 29, Appl
19	90.5	1568	17	US-10-221-278-29	Sequence 29, Appl
19	90.5	1610	19	US-10-491-213-89	Sequence 89, Appl

ALIGNMENTS

RESULT 1
US-10-646-391A-29
; Sequence 29, Application US/10646391A
; Publication NO. US20040082534A1
; GENERAL INFORMATION:
; APPLICANT: Jansen, Martin
; TITLE OF INVENTION: Treatment of Melanoma by Reduction in Clusterin Levels
; FILE REFERENCE: UBC.P-035
; CURRENT APPLICATION NUMBER: US/10/646,391A
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US 60/405,193
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/319,748
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 60/408,152
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US 60/473,387
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 29
; LENGTH: 21
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: RNAi for human clusterin
US-10-646-391A-29

Query Match 100.0%; Score 21; DB 17; Length 21;
Best Local Similarity 100.0%; Pred.No. 2.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCAGCAGAGUCUUCAUCAUTT 21

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Db      1 GCAGCAGAGUCUUCAUCAUTT 21
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Query Match      90.5%; Score 19; DB 17; Length 19;
Best Local Similarity 73.7%; Pred. No. 26;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
US-10-646-436-10
; Sequence 10, Application US/10646436
; Publication No. US20040096882A1
; GENERAL INFORMATION:
; APPLICANT: Jansen, Burkhard
; APPLICANT: Gleave, Martin
; APPLICANT: Signaevsky, Maxim
; APPLICANT: Beraldi, Eliana
; APPLICANT: Trougakos, Ioannis
; APPLICANT: Gonos, Efsthios
; TITLE OF INVENTION: RNAi Probes Targeting Cancer-Related Proteins
; FILE REFERENCE: UBC.P-030
; CURRENT APPLICATION NUMBER: US/10/646,436
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US 60/405,193
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/408,152
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US 60/473,387
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 21
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: RNAi for human clusterin
US-10-646-436-10

Query Match      100.0%; Score 21; DB 17; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GCAGCAGAGUCUUCAUCAUTT 21
|||||
Db      1 GCAGCAGAGUCUUCAUCAUTT 21
|||||

RESULT 3
US-10-646-391A-42/c
; Sequence 42, Application US/10646391A
; Publication No. US20040082534A1
; GENERAL INFORMATION:
; APPLICANT: Jansen, Burkhard
; APPLICANT: Gleave, Martin
; TITLE OF INVENTION: Treatment of Melanoma by Reduction in Clusterin Levels
; FILE REFERENCE: UBC.P-035
; CURRENT APPLICATION NUMBER: US/10/646,391A
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US 60/405,193
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/319,748
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 60/408,152
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US 60/473,387
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 42
; LENGTH: 19
; TYPE: RNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: RNAi for human clusterin
US-10-646-391A-42

Query Match      90.5%; Score 19; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GCAGCAGAGUCUUCAUCAU 19
|||||
Db      1 GCAGCAGAGUCUUCAUCAU 19
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RESULT 5
US-10-646-436-67/c
; Sequence 67, Application US/10646436
; Publication No. US20040096882A1
; GENERAL INFORMATION:
; APPLICANT: Jansen, Burkhard
; APPLICANT: Gleave, Martin
; APPLICANT: Signaevsky, Maxim
; APPLICANT: Beraldi, Eliana
; APPLICANT: Trougakos, Ioannis
; APPLICANT: Gonos, Efsthios
; TITLE OF INVENTION: RNAi Probes Targeting Cancer-Related Proteins
; FILE REFERENCE: UBC.P-030
; CURRENT APPLICATION NUMBER: US/10/646,436
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US 60/405,193
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/408,152
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US 60/473,387
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 67
; LENGTH: 19
; TYPE: RNA
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; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: RNAi for human clusterin
US-10-646-436-67

Query Match 90.5%; Score 19; DB 17; Length 19;
Best Local Similarity 73.7%; Pred. No. 26;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGCAGAGUCUUCAU 19
Db 19 GCAGCAGAGTCTTCATCAT 1

RESULT 6

US-10-646-436-68
; Sequence 68, Application US/10646436
; Publication No. US20040096882A1
; GENERAL INFORMATION:
; APPLICANT: Jansen, Burkhard
; APPLICANT: Gleave, Martin
; APPLICANT: Sigmaevsky, Maxim
; APPLICANT: Beraldi, Eliana
; APPLICANT: Trougakos, Ioannis
; APPLICANT: Gonos, Efstathios
; TITLE OF INVENTION: RNAi Probes Targeting Cancer-Related Proteins
; FILE REFERENCE: UBC.P-030
; CURRENT APPLICATION NUMBER: US/10/646,436
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US 60/405,193
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/408,152
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US 60/473,387
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 68
; LENGTH: 19
; TYPE: RNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: RNAi fo rhuman clusterin
US-10-646-436-68

Query Match 90.5%; Score 19; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGCAGAGUCUUCAU 19
Db 1 GCAGCAGAGUCUUCAU 19

RESULT 7

US-09-944-326-4
; Sequence 4, Application US/09944326
; Patent No. US20020128220A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY
; FILE REFERENCE: UBC.P-020-2
; CURRENT APPLICATION NUMBER: US/09/944,326
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 60/121,726
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 09/913,325
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 4
; LENGTH: 21
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; OTHER INFORMATION: antisense TRPM-2 ODN
US-09-944-326-4

Query Match 90.5%; Score 19; DB 9; Length 21;
Best Local Similarity 73.7%; Pred. No. 27;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGCAGAGUCUUCAU 19
Db 3 GCAGCAGAGTCTTCATCAT 21

RESULT 8

US-09-967-726A-4
; Sequence 4, Application US/09967726A
; Publication No. US20030158130A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; APPLICANT: Zellweger, Tobias
; TITLE OF INVENTION: Chemo- and Radiation-Sensitization of Cancer by Antisense TRPM-2
; TITLE OF INVENTION: Oligonucleotides
; FILE REFERENCE: UBC.P-022
; CURRENT APPLICATION NUMBER: US/09/967,726A
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 21
; TYPE: DNA
; ORGANISM: human
; OTHER INFORMATION: human
US-09-967-726A-4

Query Match 90.5%; Score 19; DB 10; Length 21;
Best Local Similarity 73.7%; Pred. No. 27;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGCAGAGUCUUCAU 19
Db 3 GCAGCAGAGTCTTCATCAT 21

RESULT 9

US-10-080-794-4
; Sequence 4, Application US/10080794
; Publication No. US20030166591A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; APPLICANT: Monia, Brett P.
; TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY USING AN OLIGONUCLEOTIDE
; TITLE OF INVENTION: HAVING 2'-O-(2-METHOXY)ETHYL MODIFICATIONS
; FILE REFERENCE: UBC.P-020-3
; CURRENT APPLICATION NUMBER: US/10/080,794
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/121,726
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 09/913,325
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 09/944,326
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4

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; LENGTH: 21
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; OTHER INFORMATION: antisense TRPM-2 ODN
US-10-080-794-4

Query Match          90.5%; Score 19; DB 16; Length 21;
Best Local Similarity 73.7%; Pred. No. 27;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGCAGAGUCUUCAUCAU 19
Db 3 GCAGCAGAGTCTTCATCAT 21

RESULT 10
US-10-646-391A-4
; Sequence 4, Application US/10646391A
; Publication No. US20040082534A1
; GENERAL INFORMATION:
; APPLICANT: Jansen, Burkhard
; TITLE OF INVENTION: Treatment of Melanoma by Reduction in Clusterin Levels
; FILE REFERENCE: UBC P-035
; CURRENT APPLICATION NUMBER: US/10/646,391A
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US 60/405,193
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/319,748
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 60/408,152
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US 60/473,387
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 21
; TYPE: DNA
; ORGANISM: human
US-10-646-391A-4

Query Match          90.5%; Score 19; DB 17; Length 21;
Best Local Similarity 73.7%; Pred. No. 27;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGCAGAGUCUUCAUCAU 19
Db 3 GCAGCAGAGTCTTCATCAT 21

RESULT 11
US-10-646-391A-28/c
; Sequence 28, Application US/10646391A
; Publication No. US20040082534A1
; GENERAL INFORMATION:
; APPLICANT: Jansen, Burkhard
; TITLE OF INVENTION: Treatment of Melanoma by Reduction in Clusterin Levels
; FILE REFERENCE: UBC P-035
; CURRENT APPLICATION NUMBER: US/10/646,391A
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US 60/405,193
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/319,748
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 60/408,152
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US 60/473,387
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
US-10-646-436-9/c
; Sequence 9, Application US/10646436
; Publication No. US2004009882A1
; GENERAL INFORMATION:
; APPLICANT: Jansen, Burkhard
; APPLICANT: Gleave, Martin
; APPLICANT: Signaevsky, Maxim
; APPLICANT: Beraldi, Eliana
; APPLICANT: Trougakos, Ioannis
; APPLICANT: Gonos, Efstathios
; TITLE OF INVENTION: RNAi Probes Targeting Cancer-Related Proteins
; FILE REFERENCE: UBC P-030
; CURRENT APPLICATION NUMBER: US/10/646,436
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US 60/405,193
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/408,152
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US 60/473,387
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 21
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: RNAi for human clusterin
US-10-646-436-9

Query Match          90.5%; Score 19; DB 17; Length 21;
Best Local Similarity 73.7%; Pred. No. 27;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGCAGAGUCUUCAUCAU 19
Db 19 GCAGCAGAGTCTTCATCAT 1

RESULT 13
US-10-828-394-5
; Sequence 5, Application US/10828394
; Publication No. US20040220131A1
; GENERAL INFORMATION:
; APPLICANT: Jackson, John
; APPLICANT: Burt, Helen
; APPLICANT: Springate, Christopher
; APPLICANT: Gleave, Martin
; TITLE OF INVENTION: Method for Treatment of Cancerous Angiogenic Disorders
; FILE REFERENCE: UBC P-033
; CURRENT APPLICATION NUMBER: US/10/828,394
; CURRENT FILING DATE: 2004-04-19
; PRIOR APPLICATION NUMBER: US 60/464,159
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 23
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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 21
; TYPE: DNA
; ORGANISM: human
US-10-828-394-5

Query Match          90.5%; Score 19; DB 18; Length 21;
Best Local Similarity 73.7%; Pred. No. 27;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGCAGAGUCUUCAU 19
Db 3 GCAGCAGAGTCTTCATCAT 21

RESULT 14
US-10-828-395-5
; Sequence 5, Application US/10828395
; Publication No. US20040224914A1
; GENERAL INFORMATION:
; APPLICANT: Jackson, John
; APPLICANT: Burt, Helen
; APPLICANT: Springate, Christopher
; APPLICANT: Gleave, Martin
; TITLE OF INVENTION: Method for Treatment of Angiogenic Disorders
; FILE REFERENCE: UBC.P-032
; CURRENT APPLICATION NUMBER: US/10/828,395
; CURRENT FILING DATE: 2004-04-19
; PRIOR APPLICATION NUMBER: US 60/464,159
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: US 60/464,160
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 21
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US-10-828-395-5
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Db 3 GCAGCAGAGTCTTCATCAT 21
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US-10-646-436-66/C
; Sequence 66, Application US/10646436
; Publication No. US20040096882A1
; GENERAL INFORMATION:
; APPLICANT: Jansen, Burkhard
; APPLICANT: Gleave, Martin
; APPLICANT: Signaevsky, Maxim
; APPLICANT: Beraldi, Eliana
; APPLICANT: Trougakos, Ioannis
; APPLICANT: Gonos, Efstathios
; TITLE OF INVENTION: RNAi Probes Targeting Cancer-Related Proteins
; FILE REFERENCE: UBC.P-030
; CURRENT APPLICATION NUMBER: US/10/646,436
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US 60/405,193
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/408,152
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US 60/473,387
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.2
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; SEQ ID NO 66
; LENGTH: 23
; TYPE: DNA
; ORGANISM: human
US-10-646-436-66

Query Match          90.5%; Score 19; DB 17; Length 23;
Best Local Similarity 73.7%; Pred. No. 27;
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QY 1 GCAGCAGAGUCUUCAU 19
Db 21 GCAGCAGAGTCTTCATCAT 3

Search completed: May 24, 2005, 00:29:27
Job time : 343 secs
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